

Parameters to *codeml*

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noisy      = 0          * 0,1,2,3,9: how much rubbish on the screen
verbose    = 0          * 1: detailed output, 0: concise output
runmode    = -2        * 0: user tree; 1: semi-automatic; 2: automatic *3: StepwiseAddition;
(4,5):PerturbationNNI; -2: pairwise

cleandata   = 1          * "I added on 07/07/2004" Mikita Suyama

seqtype = 1 * 1:codons; 2:AAs; 3:codons-->AAs CodonFreq = 2 * 0:1/61 each, 1:F1X4, 2:F3X4,
3:codon table
model = 2 * models for codons: * 0:one, 1:b, 2:2 or more dN/dS ratios for branches

NSsites    = 0          * dN/dS among sites. 0:no variation, 1:neutral, 2:positive
icode      = 0          * 0:standard genetic code; 1:mammalian mt; 2-10:see below
Mgene      = 0          * 0:rates, 1:separate; 2:pi, 3:kappa, 4:all

fix_kappa  = 0          * 1: kappa fixed, 0: kappa to be estimated
kappa      = 2          * initial or fixed kappa
fix_omega  = 0          * 1: omega or omega_1 fixed, 0: estimate
omega      = 1          * initial or fixed omega, for codons or codon-transltd AAs

fix_alpha  = 1          * 0: estimate gamma shape parameter; 1: fix it at alpha
alpha      = .0         * initial or fixed alpha, 0:infinity (constant rate)
Malpha     = 0          * different alphas for genes
ncatG      = 4          * # of categories in the dG or AdG models of rates

clock      = 0          * 0: no clock, unrooted tree, 1: clock, rooted tree
getSE      = 0          * 0: don't want them, 1: want S.E.s of estimates
RateAncestor = 0        * (1/0): rates (alpha>0) or ancestral states (alpha=0)
method     = 0          * 0: simultaneous; 1: one branch at a time

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